

Dioxygenases Present in Phenanthrene and Fluoranthene Degradation by Bacterial and Fungal Co-cultures

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Background/Objectives. The toxicity and deleterious effects of polycyclic aromatic hydrocarbons (PAHs) necessitate their removal from the ecosystem. This removal is better achieved via biodegradation of PAHs using co-cultures because it promises a complete degradation of PAHs using the synergistic metabolic machineries of the cultures comprising the consortium. Furthermore, degradation product of one organism serves as the substrate of degradation for the other organism in the consortium. Biodegradation are efficiently monitored by the degradation genes, which include polycyclic aromatic hydrocarbon ring hydroxylating dioxygenase (PAH-RHD) genes. The PAH-RHD contains alpha subunit that is the catalytic as well as substrate-determining domain.

Approach/Activities. A potouse microcosm experiment was set up in which sterile agricultural soil was contaminated by 0.1 g of each of phenanthrene and fluoranthene per kg of soil. The contaminated soil was potted and maintained at water holding capacity of 60 – 80% of the field capacity. Pine plant, bacteria and ectomycorrhizal fungi (ECMF) were introduced into the pots in six different treatment combinations which included the control. Each treatment was replicated 18 times to facilitate destructive sampling at three different times. The expression of PAH degradation genes, including oxygenases, laccases and peroxidases, were investigated for each treatment by using specific primers. Polycyclic aromatic hydrocarbon ring hydroxylating dioxygenase (PAH-RHD) genes were amplified and cloned. Samples of each treatment were also analyzed for phenanthrene and fluoranthene by GC-MS.

Results/Lessons Learned. PAH-RHD genes were amplified in all treatments but not in the control treatments without PAHs. The cloned PAH-RHD genes were identified as being homologous at sequence similarity of 98% and above to the alpha subunit of several bacterial hydroxylating dioxygenases. Biodegradation was demonstrated by the relative abundance of PAH-RHD genes as well as dissipation of PAHs in the various treatments. These findings suggest the potential of the combination of organisms to degrade typical PAHs which are important pollutants worldwide.